

Fig.1A.

	LIGAND (E2)	AAD-ER		ADD-ER Mut	
		-	100nM	-	100nM
DBD	20-29	0.4	0.5	0.3	0.6
	132-139	2	83	3	2
	184-192	3	583	2	3
	266-273	0.4	34	0.9	0.6
	379-387	0.6	208	0.9	0.9
DBD-RIP140	498-506	0.5	82	0.7	0.8
	712-719	9	1605	10	11
	818-825	2	598	1	2
	935-942	0.7	715	1	1
	935-942	0.7	498	0.9	0.8
DBD-SRC1a	45-53	0.2	77	0.4	0.4
	111-118	0.5	3.3	0.9	0.6
	632-640	0.5	0.6	0.6	0.8
	689-696	0.5	678	0.7	0.8
	748-755	1	1632	1	0.8
DBD-CBP	912-920	3	366	3	4
	1434-1441	0.4	0.7	0.7	0.8
	68-75	3	373	3	3
		0.3	28	0.4	0.5

Fig.1B.

DBD-RIP140 935-943

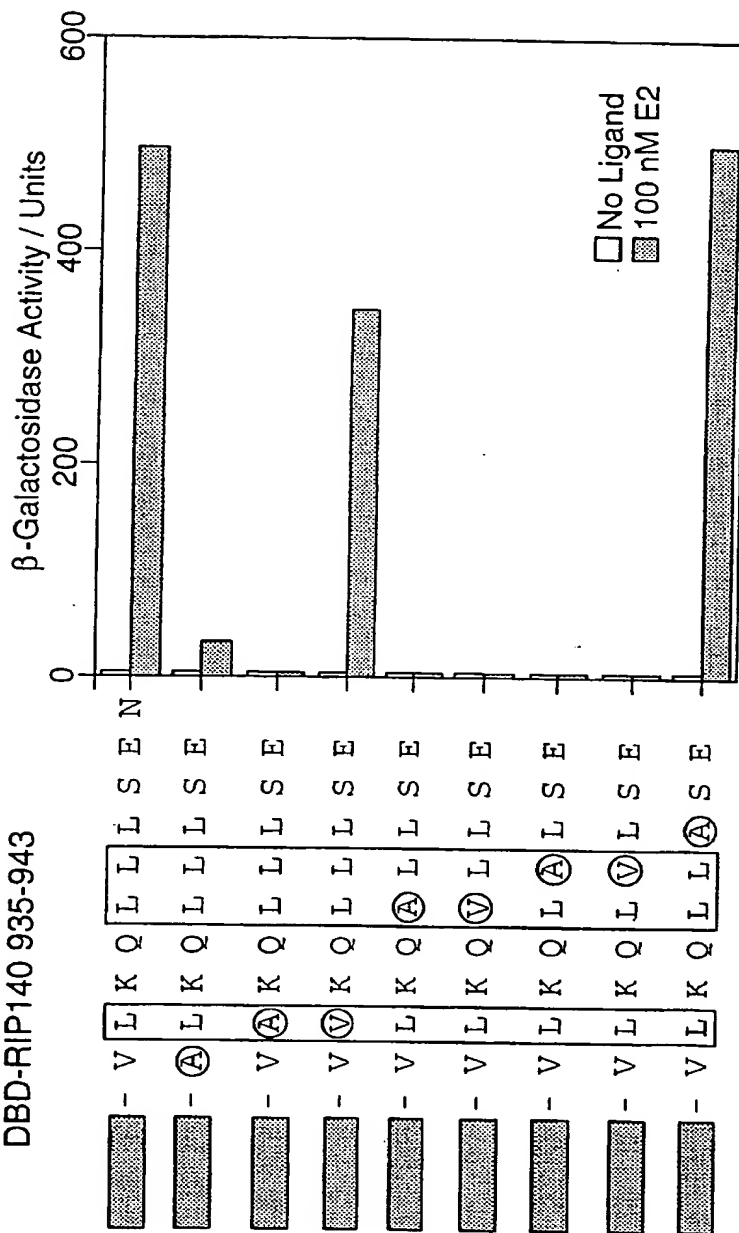


Fig.2A.

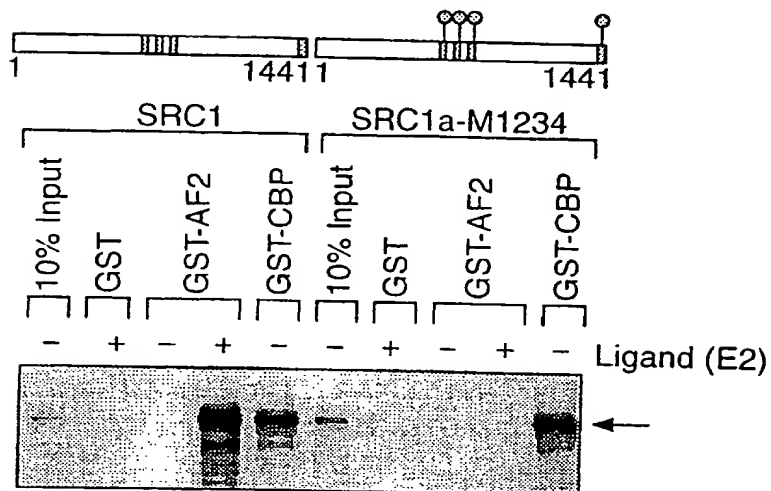
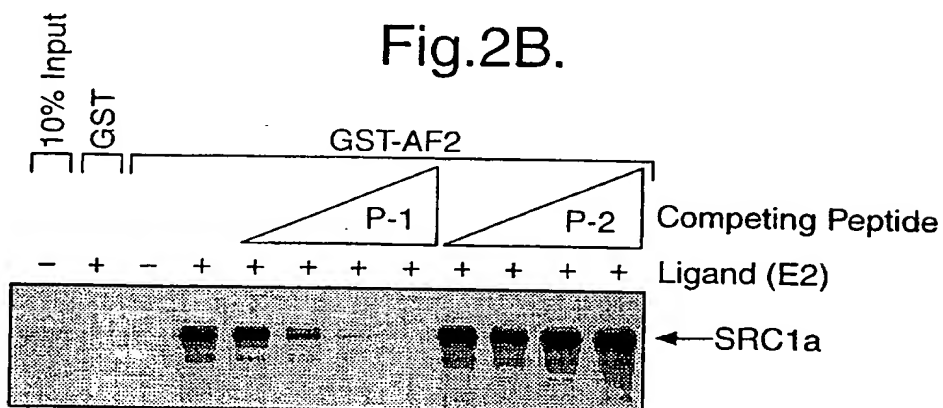


Fig.2B.



P-1 PQAQQKSL LQQ LLT  
P-2 PQAQQKSL LQQ AAT

Fig.2C.

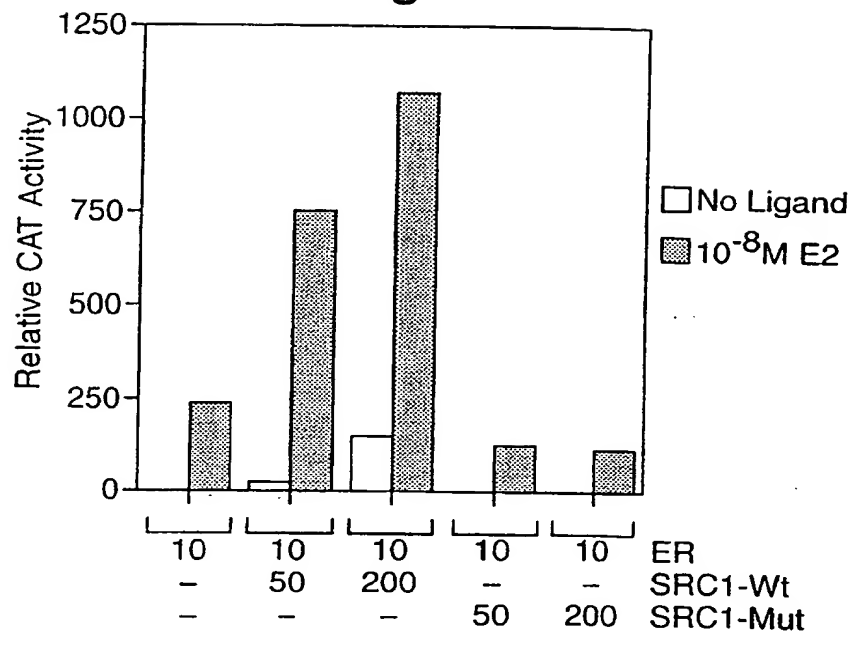


Fig.3A.

		*		*	*						
	Y	L	E	G	L	L	M	H	Q	A	A
	L	L	A	S	L	L	Q	S	E	S	S
	H	L	K	T	L	L	K	K	S	K	V
RIP140	Q	L	A	L	L	L	S	S	E	A	H
	L	L	L	H	L	L	K	S	Q	T	I
	V	L	Q	L	L	L	G	H	K	N	E
	V	L	Q	L	L	L	G	N	P	K	G
	L	L	S	R	L	L	R	Q	N	Q	D
	V	L	K	Q	L	L	L	S	E	N	C
	K	L	V	Q	L	L	T	T	T	A	E
SRC1a	I	L	H	R	L	L	Q	E	G	S	P
	L	L	R	Y	L	L	D	K	D	E	K
	L	L	Q	Q	L	L	T	E			
											1434-1441
	K	L	L	Q	L	L	T	T	K	S	D
TIF2	I	L	H	R	L	L	Q	D	S	S	S
	L	L	R	Y	L	L	D	K	D	D	T
											744-754
	Q	L	S	E	L	L	R	G	G	S	G
CBP	Q	L	V	L	L	L	H	A	H	K	C
											68-78
	Q	L	S	E	L	L	R	G	S	S	P
p300	Q	L	V	L	L	L	H	A	H	K	C
											341-351
	I	L	T	S	L	L	L	N	S	S	Q
TIF1											722-732
	M	L	M	N	L	L	K	D	N	P	A
Trip2											23-33
	T	L	R	S	L	L	L	N	P	H	L
Trip3											97-107
	R	L	A	V	L	L	P	G	R	H	P
Trip4											36-46
	E	L	H	N	L	L	E	V	V	S	Q
Trip5											26-36
	T	L	R	D	L	L	T	T	T	A	G
Trip8											36-46
	F	L	D	F	L	L	G	F	S	A	G
Trip9	V	L	E	L	L	L	R	A	G	A	N
	I	L	A	R	L	L	R	A	H	G	A
											73-83
											256-266
											288-298

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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Fig.3B.

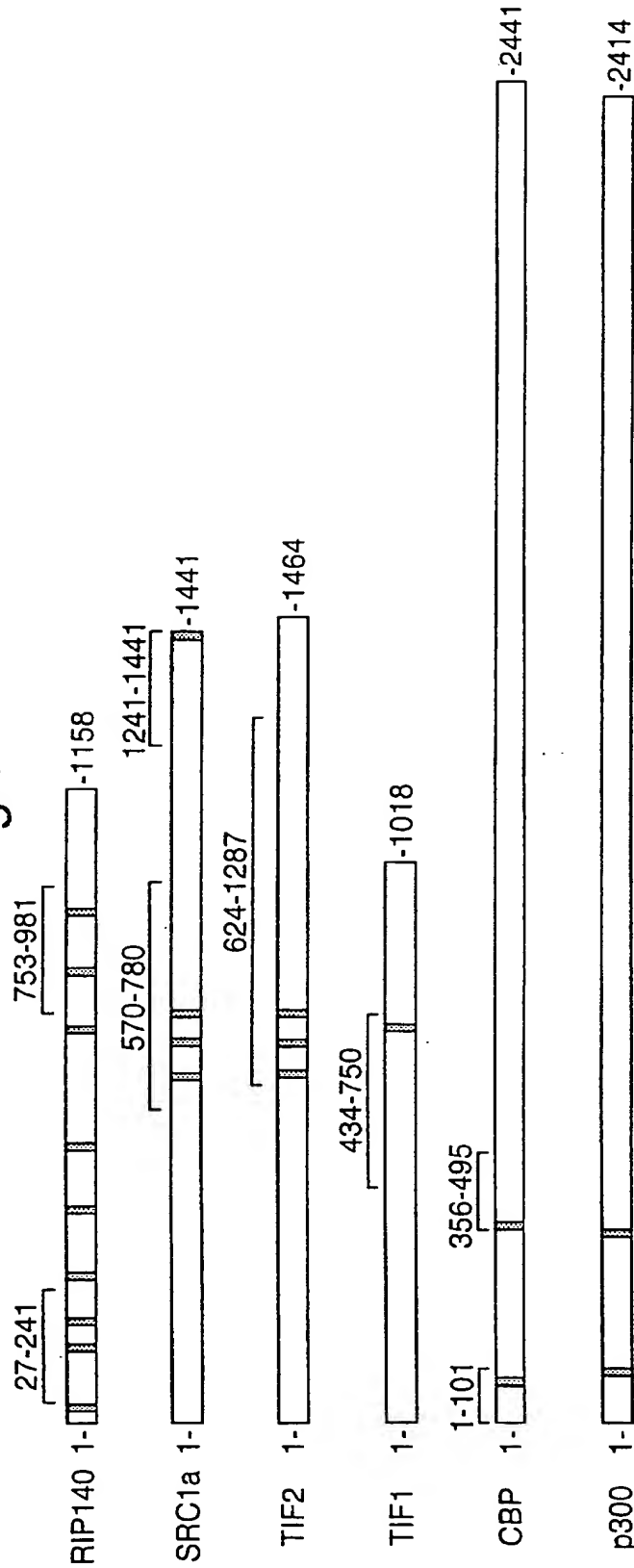




Fig.5.

